Claims

We claim:

1. An array comprising polynucleotide probes, capable of hybridizing to nucleic acid molecules of one or more of the genes in Table 2 or 3, hybridized to nucleic acids derived from one or more breast cancer cell.

2. The array of claim 1 wherein said one or more breast cancer cell is ER+.

3. The array of claim 1 wherein said nucleic acids derived from one or more breast cancer cells are prepared by mRNA amplification.

4. The array of claim 1 wherein said nucleic acids derived from one or more breast cancer cells are cDNA.

5. The array of claim 1 wherein said one or more ER+ cells are from a section of tissue from a subject or are microdissected from said section.

6. A method to determine the survival outcome of a breast cancer afflicted subject if treated with tamoxifen or other antiestrogen agent against breast cancer, said method comprising assaying a sample of breast cancer cells from said subject for the expression level(s) of one or more genes in Table 2 or 3.

7. The method of claim 6 wherein said expression level(s) are indicative of the probability of recurrence of cancer via metastasis.

8. The method of claim 6 wherein said antiestrogen agent against breast cancer is selected from a selective estrogen receptor modulator (SERM), selective estrogen receptor downregulator (SERD), or aromatase inhibitor (AI).

9. The method of claim 6 wherein said sample of breast cancer cells is ER+.

10. The method of claim 6 wherein said assaying for the expression level of one or more genes comprises detection of nucleic acids prepared by mRNA amplification from said sample of breast cancer cells.

11. The method of claim 6 wherein said assaying for the expression level of one or more genes comprises detection of nucleic acids from said sample of breast cancer cells by quantitative PCR.

12. The method of claim 6 wherein said assaying for the expression level of one or more genes comprises detection of proteins encoded by said genes or proteolytic fragments of said proteins.

13. The method of claim 12 wherein said detection of proteins or proteolytic fragments thereof comprises detection thereof in the blood of said subject or in breast cancer epithelial cells enriched from the blood of said subject.

14. A method of determining prognosis of a subject having breast cancer if treated with tamoxifen or another antiestrogen agent against breast cancer, or of a subject afflicted with breast cancer and treated with tamoxifen or another antiestrogen agent against breast cancer, said method comprising:

assaying for the expression level(s) of one or more genes in Table 2 or 3 from a breast cancer cell sample from said subject.

15. The method of claim 14 wherein said expression level(s) are indicative of the probability of recurrence of cancer via metastasis.

16. The method of claim 14 wherein said antiestrogen agent against breast cancer is selected from a selective estrogen receptor modulator (SERM), selective estrogen receptor downregulator (SERD), or aromatase inhibitor (AI).

17. The method of claim 14 wherein said sample of breast cancer cells is ER+.

18. The method of claim 14 wherein said assaying for the expression level of one or more genes comprises detection of nucleic acids prepared by mRNA amplification from said sample of breast cancer cells.

19. The method of claim 14 wherein said assaying for the expression level of one or more genes comprises detection of nucleic acids from said sample of breast cancer cells by quantitative PCR.

20. The method of claim 14 wherein said assaying for the expression level of one or more genes comprises detection of proteins encoded by said genes or proteolytic fragments of said proteins.

21. The method of claim 20 wherein said detection of proteins or proteolytic fragments thereof comprises detection thereof in the blood of said subject or in breast cancer epithelial cells enriched from the blood of said subject.

22. The method of claim 14 wherein said sample is obtained by a minimally invasive technique or selected from core biopsy, excisional biopsy, a ductal lavage sample, a fine needle aspiration sample, or cells microdissected from said sample.

23. A method to determine therapeutic treatment for a breast cancer patient based upon said patient's expected response or lack of response to treatment with tamoxifen or another antiestrogen agent against breast cancer, said method comprising

determining an expected response or non-response to treatment with tamoxifen or another antiestrogen agent against breast cancer for said patient by assaying a sample of breast cancer cells from said patient for the expression level(s) of one or more one genes in Table 2 or 3; and

selecting the appropriate treatment for a patient with such a survival outcome.

24. The method of claim 23 wherein said expression level(s) are indicative of the probability of recurrence of cancer via metastasis.

25. The method of claim 24 wherein said antiestrogen agent against breast cancer is selected from a selective estrogen receptor modulator (SERM), selective estrogen receptor downregulator (SERD), or aromatase inhibitor (AI).

26. The method of claim 24 wherein said sample of breast cancer cells is ER+.

27. The method of claim 24 wherein said assaying for the expression level of one or more genes comprises detection of nucleic acids prepared by mRNA amplification from said sample of breast cancer cells.

28. The method of claim 24 wherein said assaying for the expression level of one or more genes comprises detection of nucleic acids from said sample of breast cancer cells by quantitative PCR.

29. The method of claim 24 wherein said assaying for the expression level of one or more genes comprises detection of proteins encoded by said genes or proteolytic fragments of said proteins.

30. The method of claim 29 wherein said detection of proteins or proteolytic fragments thereof comprises detection thereof in the blood of said subject or in breast cancer epithelial cells enriched from the blood of said subject.

31. The method of claim 24 wherein said sample is obtained by a minimally invasive technique or selected from core biopsy, excisional biopsy, a ductal lavage sample, a fine needle aspiration sample, or cells microdissected from said sample.

32. A method to determine the survival outcome of a human subject having breast cancer if treated with tamoxifen or another antiestrogen agent against breast cancer, said method comprising assaying a sample of breast cells from said subject for expression of one or more human HOXB13, IL17BR or CACNA1D sequences or another sequence the expression of which is correlated with their expression in breast cancer cells,

wherein underexpression of HOXB13 sequences is indicative of responsiveness, and overexpression of IL17BR and/or CACNA1D sequences is indicative of non-responsiveness, to treatment with tamoxifen or another antiestrogen agent against breast cancer.

33. The method of claim 32 wherein said antiestrogen agent against breast cancer is selected from a selective estrogen receptor modulator (SERM), selective estrogen receptor downregulator (SERD), or aromatase inhibitor (AI).

34. The method of claim 32 wherein said sample of breast cancer cells is ER+ or is obtained by a minimally invasive technique or selected from core biopsy, excisional biopsy, a ductal lavage sample, a fine needle aspiration sample, or cells microdissected from said sample..

35. The method of claim 32 wherein said assaying for expression comprises detection of nucleic acids prepared by mRNA amplification from said sample of breast cancer cells or detection of nucleic acids from said sample of breast cancer cells by quantitative PCR.

36. The method of claim 32 wherein said assaying for expression comprises detection of proteins encoded by said genes or proteolytic fragments of said proteins.

37. The method of claim 36 wherein said detection of proteins or proteolytic fragments thereof comprises detection thereof in the blood of said subject or in breast cancer epithelial cells enriched from the blood of said subject.

38. The method of claim 32 wherein said assaying is by hybridization to a polynucleotide comprising sequences of at least 15 nucleotides from the 3' untranslated region, the coding region, or the 5' untranslated region, of human HOXB13, IL17BR or CACNA1D sequences.

39. The method of claim 32 wherein said assaying is for lack of underexpression of HOXB13 sequences or lack of overexpression of IL17BR or CACNA1D sequences.

40. The method of claim 32 wherein said assaying comprises a ratio of the expression level of a HOXB13 sequence to the expression level of an IL17BR or CACNA1D sequence.

41. The method of claim 39 wherein said assaying comprises a ratio of the expression level of a HOXB13 sequence to the expression level of an IL17BR or CACNA1D sequence as an indicator of non-responsiveness to tamoxifen or another antiestrogen agent against breast cancer.

42. The method of claim 32 wherein said assaying for expression comprises assaying for inactivation or methylation of HOXB13, IL17BR or CACNA1D sequences.

43. The method of claim 32 wherein said assaying for HOXB13 expression comprises detection of HOXB13, IL17BR or CACNA1D mRNA degradation.

45. A population of singled stranded nucleic acid molecules comprising one or both strands of a human IL17BR or CACNA1D or HOXB13 sequence wherein at least a portion of said population is hybridized to one or both strands of a nucleic acid molecule quantitatively amplified from RNA of a breast cell.

46. The population of claim 45 wherein the population is immobilized on a solid support, such as a microarray.

47. The population of claim 45 wherein said nucleic acid molecules amplified from a breast cell are amplified RNA molecules.

48. The population of claim 45 wherein said breast cell is ER+.

49. A method to determine the survival outcome of a human subject having breast cancer if treated with tamoxifen or another antiestrogen agent against breast cancer, said method comprising assaying a sample of breast cells from said subject for expression of a sequence selected from SEQ ID NOs: 8, 9, 11-17, or 32-34.

50. A method to determine the survival outcome of a human subject having breast cancer if treated with tamoxifen or another antiestrogen agent against breast cancer, said method comprising assaying a sample of breast cells from said subject for expression of a sequence selected from SEQ ID NOS: 10 18-31, or 35-37.

51. A method of predicting responsiveness or lack thereof in a breast cancer afflicted subject to treatment with tamoxifen or another o